



Second Corrected Sequence Listing 5-2002

SEQUENCE LISTING

<110> Novartis AG
Novartis Research Foundation

<120> Gene involved in epigenetic gene silencing

<130> S-31005A

<140>
<141>

<150> GB 9914623.5
<151> 1999-06-23

<160> 33

<170> PatentIn Ver. 2.1

<210> 1
<211> 10329
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> intron
<222> (1009)..(1295)

<220>
<221> intron
<222> (2551)..(2673)

<220>
<221> intron
<222> (2753)..(2867)

<220>
<221> intron
<222> (3114)..(3506)

<220>
<221> intron
<222> (3681)..(3973)

<220>
<221> intron
<222> (4896)..(4975)

<220>
<221> intron
<222> (5218)..(5777)

<220>
<221> intron
<222> (5883)..(6082)

<220>
<221> intron
<222> (7481)..(7615)

<220>
<221> intron

Second Corrected Sequence Listing 5-2002

<222> (7772)..(7914)

<220>

<221> intron

<222> (8071)..(8153)

<220>

<221> intron

<222> (8319)..(8451)

<220>

<221> intron

<222> (8630)..(8718)

<220>

<221> intron

<222> (8919)..(9000)

<220>

<221> intron

<222> (9212)..(9284)

<400> 1

aatattttaag	tttggtttat	attcttttcta	gtaatctttg	aaatattgta	agagataatg	60
cttctaataa	ataacattgg	atttattgga	attaatgtat	tgaaaaaact	atgcaaatac	120
tacagtgtat	tttggaaacga	ccaaaatgat	atatgtaaac	tttcgttcta	gtcttctaca	180
tagtgtaata	ggatagcggga	caagggttgat	cgactctaaa	cattatgggt	acgtaattcc	240
gcagtgggta	cagtctactg	tcgaggccaa	actggtaatt	aaacgtttga	agtttagaga	300
aatattttga	tgatgagtac	cacaatcaaa	gatgataggt	gttaatcact	gtaaaaatgt	360
tgattgaata	ctacgaatgc	agaacatata	catattttta	atctcttttg	aatttttggt	420
tttgttttta	tcatttttga	atacacgaag	agctcagtta	tatttcatat	tgtatatgaa	480
tttgtttctat	ttaatcttca	attctagcaa	catactctta	tgctaattcg	tttcataatt	540
tagtatagta	taaaaattac	aaatttcaaa	acaaactata	agtaatatatac	taacatagtc	600
gggtgaacat	ttcgttaatt	tcacataaca	tatgttaatt	acatatgtac	actatttttg	660
aagtattttta	taacttaaaa	tatataaatt	taaatctaag	aaatcacaaag	catgagtttt	720
tccttccggt	aatcgtaaaa	tcaaaaatcg	ctcgcctcgag	aaacgccgggt	gctagaagag	780
gaaagtaccg	tacataatcc	tgcaaaccca	attctcgtct	tcttcaaact	cagttttccg	840
aaaccccaaa	caccgcgagg	attgcatggc	ctgaagaacc	acttaatcga	gaattgtgct	900
gggaattctca	aattttccct	cgcgtttttc	tttcacactc	tcggaatcgg	aaatttccac	960
caagctccgt	caagcgatag	attctgacaa	ttacacactt	tcgcgcaggt	atgcttccct	1020
ccctgtttta	ggttgggtgt	aatctatcgg	tgaatcgaag	gttttgggcc	tcgggctttg	1080
cgtttttaggt	ttttcagaga	atcttatcta	cttggggatg	gatcttaggc	gtttgttaga	1140
tgtaactcat	tagttttgca	tataggaatt	ttgatttgaa	agttaggtcg	ccggatttgt	1200
agacattttg	tttgatggtc	ttcttcggtg	ctcacattct	ttgtttttta	gtgcttgatt	1260
tggttgctaa	ggtcctttcc	gttgctgtgct	ctcagtgaat	atgaagaaag	atgaaaagat	1320
tggtttgacg	gggagaacca	tttacaccag	atccctagca	gcttcaattc	ctgcctcagt	1380
tgaacaagaa	acccctggtt	tgaggaggtc	aagccggggg	acaccatcta	cgaaggtaat	1440
aactccagct	tctgctacta	gaaagtcaga	gagactggct	ccctcacctg	cttcagtttc	1500
aaaaaagtcc	ggtggaatcg	tcaagaattc	cacaccaagt	tctttgcgaa	ggtccaatag	1560
ggggaagact	gaagtatcct	tgcaagattc	caaaggatca	gataattcta	tcaggaaagg	1620
agatacttca	ccggaatattg	agcagagaaa	ggatagtgtt	gaagagtcga	cagataagat	1680
caagcctata	atgtcagccc	gaagttacag	ggcattgttt	agagggaagc	tcaaggaatc	1740
tgaggcatta	gttgatgctt	ccccaaatga	agaggaaacta	gtagtgtgtg	gttggttctcg	1800
ccgcatacct	gcaggcaatg	atgatgttca	aggtaaaaca	gattgtccac	cacctgcaga	1860
ttcaggatca	aaaaggctgc	cagttgacga	aactagtttg	gacaagggca	ctgattttcc	1920
tttgaaatca	gttacggaga	ccgagaagat	agtgcttgat	gcatccccc	tagttgaaac	1980
tggggatgac	agtgttatag	gttcaccatc	tgagaattta	gagacacaaa	agcttcaaga	2040
tggttaagaca	gattgttcac	cacctgcaaa	tgagaatcg	aaaacgctgc	cagttgggtga	2100
aactagttta	gaaaaagaat	atccacaaaa	gtttcaagat	gataacacag	attgtctacc	2160
acctgcaaat	gcagaatcaa	aaaggctgcc	agttggcgaa	actagtttag	aaaaggacac	2220
tgatttttct	ttgaaatcaa	ctacggagac	tggaagaatg	gttctttatg	catcccccac	2280
agttgaaact	agggatgaca	cggttatatg	ttcaccatct	acaaatttag	aaacccaaaa	2340
gcttcttgct	agtaaaactg	gcttagaaac	cgacatagtt	ttgcctttga	aaagaaaaag	2400

Second Corrected Sequence Listing 5-2002

agacactgca	gaaattgagc	tggtatgcatg	tgctacagtt	gcaaattggag	atgatcacgt	2460
tatgagttct	gatgggggtca	ttccatctcc	atctgggtgc	aaaaatgata	atcgacctga	2520
aatgtgcaac	acgtgtaaaa	aacggcaaaa	gtaagagttt	ttttagtggt	gtctgtctat	2580
tgaaacgatc	tgccaatggt	gaatgttggg	cagatgggtt	tgattcttag	gatatatgtt	2640
ctgtattgta	atgagttggt	caaaattttg	aagggctaac	ggtgattgtc	aaaataggag	2700
tgtttgctcc	tgcatgtgcc	agccagttga	agaatctgat	aacgtgacac	aggttgggtt	2760
ctaattactt	tcggagaccc	gttaatcagt	ggactcttaa	atagttagat	actagattta	2820
cttatccttt	tacttgaat	ctgcaattct	attttgcat	tgattaggat	atgaaagaaa	2880
ctggaccagt	tacgagcaga	gaatatgagg	agaacgggca	aatacaacat	ggtaaatcaa	2940
gtgatcccaa	attctattct	tcgggtgacc	cagagtattg	ggttcctgtg	cagctatcag	3000
atgtacagct	ggagcaatac	gtcagactc	tcttctccaa	atccttatct	ctttcttcac	3060
tttcgaagat	tgatcttgga	gctctagaag	aaactctcaa	ttctgtaaga	aaagtaagtt	3120
acttgatttt	aaaaacactt	attcttcaat	gcacttggtga	gttaagtacc	cagttattac	3180
tggtgataag	ataaagaaa	caatagaaaa	attgataagg	tgttcaccgc	attgcagcca	3240
aaaaaacgat	atgctgttcc	atgctttcaa	gaggttgc	catagggtgt	atgcctttct	3300
gtttgatgtt	tggttagagca	aagggttttg	gtctatttgt	tttatgcttt	tttgaaacac	3360
atagaacctg	gcaaacttga	cagttttggg	gttgcttaga	tatacgacta	ttgtcgggtca	3420
gcatcacatt	ttctcaaggc	ctctttctgc	atgttaatgt	gtgaatatat	taaaatcttc	3480
tttatgtgtt	tgcaacttgt	tgacagacct	gtgaccatcc	atacgttatg	gatgcattct	3540
tgaacaact	gctcaccaag	aatctggagt	tgcatgaaat	cctggatgta	gaaattaaag	3600
cgagcgggaa	acttcacctc	cttgataaaa	tgcttactca	tataaaaaag	aatgggttaa	3660
aagcagttgt	cttctaccag	gtgcattttc	tattacttgc	gaatgtgaat	agctctatgt	3720
ttgtcatgaa	tacgtcactt	tgtgcattct	caatatatgt	gcattttctt	tttgacaatg	3780
gaattctgtc	ttgtattgaa	atttgagtgg	gatgaaagta	tgctttttat	cgtgcaatta	3840
tgaagtgtaa	gttagccttc	agcagtcagc	tagcattatg	agatatgctg	aactaaaatg	3900
tttcttttct	cttcttttct	tttcgttata	tgtgcctcat	gtatgtttga	attacagttt	3960
ttattttcag	caggcaacac	aaacccttga	agggttctg	cttggttaata	ttctcgaaga	4020
ttttgtgggt	caaagatttg	gtccaaaatc	ttatgagcat	gggatataat	cctcaaagaa	4080
gaactccgct	ataaacaatt	tcaacaagga	gagtcaatgc	tgtgttctgc	tgttggaaac	4140
acgtgcctgc	agtcaaacca	ttaaactctt	gcgagctgat	gctgtttatt	tttttggaag	4200
cagcttgaat	ccatcgcatg	atgttaagca	cgtagagaag	ataaaaatcg	agtcattgtt	4260
tgaagaact	aagatattcc	gattgtactc	agtatgtaca	gttgaagaaa	aagccctgat	4320
cttggtcagg	caaaaatagc	ggcaaaataa	agctgtagag	aacctaaacc	gctctctcac	4380
gcacgcactg	ctcatgtggg	gggcgtcata	cttattttgat	aaactggatc	attttcacag	4440
cagtgaact	ccagattcag	gagtttcatt	tgaacaatct	attatggacg	gcgtgattca	4500
tgaattctcg	tccatacttt	cttccaaagg	tggagaagaa	aatgaagtca	agctgtgtct	4560
acttttgtag	gccaagcatg	ctcagggaa	ttacagcagt	gattctactc	tatttggtga	4620
agaccatagt	aagttgtcag	atgaagagag	tccaaatata	ttttgggtcaa	agctgttggg	4680
gggaaaaaat	cctatgtgga	aatacccttc	agatactccc	caaagggaatc	gaaaacgagt	4740
tcagtatttt	gagggttctg	aagcgagtcc	caaaactggc	gatgggtgaa	atgcaaagaa	4800
gcgaaagaag	gcttctgatg	atgtcactga	tccccgggtc	actgatccgc	cagtagatga	4860
tgatgaaaga	aaggcctctg	ggaaggatca	catgggtaaa	atagtttaat	ttctgtctccg	4920
atacctctag	tgttcattga	ttatgcaact	actttgctga	ctatctttcc	tacaggggct	4980
ttggagtcac	aaaagtcat	aacactccag	tcctcatgta	aatcttctgg	tacagatgg	5040
acattggatg	gaaatgatgc	ttttggcttg	tattctatgg	gcagccatat	ctctggaatc	5100
ccagaggata	tgttagctag	tcaagattgg	gggaaaatac	cggatgaatc	acagaggagg	5160
ctccacactg	ttttaagacc	gaagatggca	aaactttgcc	aagttttgca	tctttcagta	5220
agtggccttt	ttcacctcca	caacttattt	tagccttgca	tatgcttata	tatagctgat	5280
tgcaactgta	gttgttacct	gatttcttgt	tacagccaaa	tgtgagagtt	ttattcttca	5340
actatatcca	tccgtttaag	catattttat	ttcttatatc	tggcttcggt	accaatgcac	5400
tgttaaaaatg	agcaactgct	gcacaaaaca	gtaggtagtt	atgtgcctca	tgctattcat	5460
tgttttattga	agcaaagaaa	tttctgtcta	ctttacatga	tccatctgtg	ggagtatata	5520
actatatata	accttaggcc	tttgtacctg	gctgatcaaa	gacatgtcaa	aagtttatct	5580
gttcgctgtt	ggtatagaaa	ctaatacagt	gtctgatgct	attttaagg	agtcttatgt	5640
cttcacatat	tggtctaata	atgtttccgc	tgctgtgtcc	atatacttct	gtgattatca	5700
cgggtgctccg	tctatacaaa	ttgtactaaa	aggatttttg	caatgtgtga	ttgggttaaca	5760
gattattttg	ttttcaggat	gcttgcaaaa	gcatggctcg	aaattttctc	gaatatgtta	5820
ttgaaaatca	ccgaatctac	gaagagccag	ccactacttt	tcaggcatte	cagatagccc	5880
tggtatgaca	gcattttact	tgataattta	tgcatgtgtt	ccttcatcat	ctgcctttgt	5940
ttagaatgtc	ctcagaaggc	agcactcctt	tagttttaac	tttccaatca	taggattcaa	6000
atatccatta	actggccttt	gatcgctgca	taatatatga	atagttgaca	tactgaatac	6060
gtttgttaata	atgcattttc	agagttggag	tgacgccttg	ttggtaaagc	aaattcttag	6120
ccacaaagaa	tctctggtcc	gtgcaaatcc	tgaattagct	ttcaaagtgc	ctagagtaga	6180

Second Corrected Sequence Listing 5-2002

ggtggattat	atattattcga	tattgtcctg	catgaagagt	ctgttcctgg	agcatacaca	6240
aggtttgcag	ttcgattgct	ttggactaa	ttctaaacag	tcagtgggta	gcacaaaact	6300
agtaaatgaa	agtctctcag	gggctacagt	gcgtgacgaa	aagattaata	cgaagtcgat	6360
gcgaaatagc	tcagagggatg	aagagtgcac	gactgagaag	agatgtagcc	attatagcac	6420
agcaacaaga	gatatcgaaa	agactattag	tggcataaaa	aagaaataca	agaagcaagt	6480
gcaaaagcct	gtacaagagc	atgaggaaaa	gaaaatggag	ctgttaaata	tgtatgcaga	6540
caagaagcag	aaacttgaaa	ctagtataag	tgtggaagca	gcagtaattc	gtattacctg	6600
ttcacggacc	agtactcaag	tgggtgatct	caaaactgctg	gatcataatt	atgaaagaaa	6660
gtttgatgaa	atcaaaaagt	agaaaaatga	atgcctcaaa	agtctggagc	aaatgcacga	6720
ggttgcaaa	aagaagtggg	ctgaggatga	agcctgttgg	attaatcgga	taaagagctg	6780
ggcagctaaa	ttaaaagttt	gtgttcccat	tcaaagtggc	aataacaagc	attttagtgg	6840
ttcatcaaac	atttcccaaa	atgctcctga	tgtacaaatt	tgcaataatg	ctaactgtga	6900
agctacttac	gctgatacga	attgcatggc	ttccaagggt	aatcaagtgc	cagaagcaga	6960
aaacacatta	ggaacatgt	cgggtggcag	cactcaacaa	gttcatgaaa	tgggtggatg	7020
aagaaatgac	gagacaatgg	atgtctcagc	tttgtctcgt	gaacagctta	caaagagcca	7080
gtccaatgag	cacgcttcta	tcactgtgcc	tgagattttg	attcctgctg	actgtcaaga	7140
ggaattttgcg	gccttgaacg	tgcatttgtc	agaagaccag	aattgtgaca	gaataacatc	7200
tgcggcatca	gatgaagatg	tttcatcaag	gggtgccagag	gtatcccagt	cactcgaaaa	7260
tctttctgcc	tcccccgagt	tttctctaaa	tagagaggag	gctttgggtt	caacagaaaa	7320
tagaagaaca	agtcatgtgg	gttttgatac	tgataacatt	ttggaccagc	agaatagaga	7380
agattgttct	cttgaccaag	agattcctga	cgagtttagcg	atgcctgtgc	aacatcttgc	7440
gtctgtggtg	gagactaggg	gtgctgctga	atctgatcag	gtacttactg	gccctgtaga	7500
atagttgatg	ccttgttcat	ttaatctttt	ctaagtgtca	ttcttgcttt	cttgaataata	7560
acgggtagtg	atcagatgtc	tttttttctc	ttattaaatt	cacttttctg	gacagtatgg	7620
tcaagatata	tgtcctatgc	cttcttcaat	ggctggaaa	caacctgacc	cagcagcaaa	7680
cactgagagc	gaaaatcttg	aagaagcaat	tgagcctcag	tctgctgggt	cagaaacagt	7740
agagactact	gattttgctg	catcacatca	gggtccctatt	gaagactttc	cttttttact	7800
agtttaaagt	tatcaatctg	tgttatgttc	attctaagtt	tccgtgagaa	aaagggtggg	7860
aaatgtgggt	actgatcaag	tctcgttgg	gttttaaata	gactcttttg	acagggtgat	7920
caagttacat	gtcctttgct	atcttcaccg	actggaaatc	agcctgcgcc	agaagcaaat	7980
attgaaggcc	aaaatatcaa	cacatcagct	gagccccatg	tagcgggtcc	agatgcagta	8040
gagagtgggt	attatgcagc	aatagatcag	gttattggct	taactaaaga	caaatgtctt	8100
ttgtttgtta	aaagtcttac	atctttgtaa	tgctcgttct	ggatatcctg	caggaaacaa	8160
tgggtgctca	ggatgcatgc	tctctgccat	ctggatcgg	tggaaactcag	tctgacctag	8220
gagcaaacat	tgagggtcaa	aatgtcacia	cagtggctca	acttcccaca	gatggatcag	8280
atgcagttgt	aaccgggtga	tctcctgtat	cagatcaggt	acctgcctct	gctcaaggac	8340
tttcttatgt	gttgggttaa	aggtctagtc	cttagtaatg	ttgaaactaa	gcaaacagtg	8400
gatagtcatc	atatgtttat	ttttgcttgt	gaatttaata	tttctggaca	gtgtgccag	8460
gatgcacttc	ctatgccatt	atcttcgcct	ggaaatcacc	ctgatacagc	agttaatatc	8520
gagggtttag	ataacacatc	agtagctgag	cctcatataa	gtggatcaga	tgcatgtgaa	8580
atggaaatgt	cagaacctgg	tccccaaagta	gagcgggtcaa	cctttgcaag	tcagtaactg	8640
ccttgggcat	ttttaagtat	cacctaggtc	gacatatgtg	attgccaaac	agctaacaag	8700
gagatgcctt	tttgtcagat	cttttccatg	aaggtggcgt	ggagcattca	gcaggtgtaa	8760
cagctcttgt	tccatcactt	cttaacaatg	gtacgggaaca	gattgccgtt	caacctgttc	8820
ctcaaatacc	tttccctgtg	ttcaacgacc	cgtttctgca	tgaactggag	aagttgcgga	8880
gagaatcaga	gaactcaaag	aagacttttg	aagaaaaagt	cagtttccct	cattaccag	8940
ttacctcttg	ttttgggtta	ttttctagct	gcccattgac	tctcagttgc	ttgtgagcag	9000
aaatcaatct	tgaagctga	actcgagagg	aagatggctg	aagtacaagc	agagtttcga	9060
agaaaatttc	atgaggtaga	agccgagcat	aacaccagaa	cgacaaagat	agagaaggat	9120
aagaatcttg	ttataatgaa	caaactgttg	gcgaatgcgt	tcttgtccaa	atgtactgac	9180
aagaaggtat	ctccctcagg	agctccaagg	ggtaagtgtc	gaataatata	gcaaattggg	9240
tttaaaaaata	aggcgacgaa	gtcataatag	cactttttct	ccaggtaaaa	ttcagcagct	9300
agcacagaga	gcagcacaag	tgagtgcact	gagaaattac	attgctcctc	agcagcttca	9360
ggcatcttct	tttctgtctc	ctgctctggt	ttcggctcct	ctgcaacttc	agcaatcatc	9420
atttctctgt	cctggctcgg	ctcctctgca	gtcctcaggca	tcttcgtttc	cttcttcagt	9480
ctctcgtcca	tcagcccttc	ttctgaattt	tgcggctctg	ccaatgcctc	agcccagaca	9540
gcctctcata	tccaacatag	ctccaactcc	atcagttact	cctgcaacaa	atccaggtct	9600
gcgttctcct	gcaccacacc	taaactcata	tagaccatcc	tcttcaactc	ccgtcgccac	9660
agctactcca	acctcgtcag	tgctcctca	agctttgaca	tattcagctg	tgtcaattca	9720
gcagcagcaa	gaacaacaac	cgcaacagag	cttgagcagt	ggattgcaga	gcaacaatga	9780
agtggtttgt	ctttctgacg	acgagtgacc	taagaggaga	gatgggttag	gtcttagtta	9840
ttgattttta	gagagttaat	aatagtatat	atatatatgt	ataagtaggt	tacctaatct	9900
ctgtcgttaa	tctaatttag	tgagtcagga	accgactcgt	tggctaagggt	ctctcctttt	9960

Second Corrected Sequence Listing 5-2002

```

gaaacgcaac gttctacttt catgtatata aatacagtct gatcacacaa cacaaattga 10020
tgattgaaaa tactactgat ttaactttat agaaaaccca aattatagag cgacaacttt 10080
ataaacatgt caaacttcga agttaaaatt taagaccca taattttaca attatagatt 10140
ttaatactcc aactattttg tgatgtttaa agaagtatcc gagtcttttc tttccagttt 10200
ccccaccgtc ccatgactcc cccagccagt agaaaaagcc aaaaaagtaa acaaaaagtc 10260
gttaaaaaag ttaaattaaa aaaaaaatag atagttgacg tttactaaag tgatttgaat 10320
tgaacaatt                                     10329

```

<210> 2
 <211> 6571
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (310)..(6312)

```

<400> 2
cacaagcatg agtttttcct tccggtaatc gtaaaatcaa aaatcgctcg ctcgagaaac 60
gccggtgcta gaagaggaaa gtaccgtaca taatcctgcg aaccaattc tcgtcttctt 120
caaactcagt tttccgaaac cccaaacacc gcgaggattg catggcctga agaaccactt 180
aatcgagaat tgtgctggaa ttctcaaatt ttccctcgcg tttttctttc acactctcgg 240
aatcggaat ttccaccaag ctccgtcaag cgatagattc tgacaattac acactttcgc 300
gcagtgaat atg aag aaa gat gaa aag att ggt ttg acg ggg aga acc att 351
      Met Lys Lys Asp Glu Lys Ile Gly Leu Thr Gly Arg Thr Ile
          1             5             10

tac acc aga tcc cta gca gct tca att cct gcc tca gtt gaa caa gaa 399
Tyr Thr Arg Ser Leu Ala Ala Ser Ile Pro Ala Ser Val Glu Gln Glu
 15             20             25             30

acc cct ggt ttg agg agg tca agc cgg ggg aca cca tct acg aag gta 447
Thr Pro Gly Leu Arg Arg Ser Ser Arg Gly Thr Pro Ser Thr Lys Val
          35             40             45

ata act cca gct tct gct act aga aag tca gag aga ctg gct ccc tca 495
Ile Thr Pro Ala Ser Ala Thr Arg Lys Ser Glu Arg Leu Ala Pro Ser
          50             55             60

cct gct tca gtt tca aaa aag tcc ggt gga atc gtc aag aat tcc aca 543
Pro Ala Ser Val Ser Lys Lys Ser Gly Gly Ile Val Lys Asn Ser Thr
          65             70             75

cca agt tct ttg cga agg tcc aat agg ggg aag act gaa gta tcc ttg 591
Pro Ser Ser Leu Arg Arg Ser Asn Arg Gly Lys Thr Glu Val Ser Leu
          80             85             90

cag agt tcc aaa gga tca gat aat tct atc agg aaa gga gat act tca 639
Gln Ser Ser Lys Gly Ser Asp Asn Ser Ile Arg Lys Gly Asp Thr Ser
 95             100             105             110

ccg gat att gag cag aga aag gat agt gtt gaa gag tcg aca gat aag 687
Pro Asp Ile Glu Gln Arg Lys Asp Ser Val Glu Glu Ser Thr Asp Lys
          115             120             125

atc aag cct ata atg tca gcc cga agt tac agg gca ttg ttt aga ggg 735
Ile Lys Pro Ile Met Ser Ala Arg Ser Tyr Arg Ala Leu Phe Arg Gly

```

140

Page 6

Second Corrected Sequence Listing 5-2002															
Gly	Asp	Asp	His	Val	Met	Ser	Ser	Asp	Gly	Val	Ile	Pro	Ser	Pro	Ser
		385					390					395			
ggg	tgc	aaa	aat	gat	aat	cga	cct	gaa	atg	tgc	aac	acg	tgt	aaa	aaa
Gly	Cys	Lys	Asn	Asp	Asn	Arg	Pro	Glu	Met	Cys	Asn	Thr	Cys	Lys	Lys
	400					405					410				1551
cgg	caa	aag	gtc	aac	ggt	gat	tgt	caa	aat	agg	agt	gtt	tgc	tcc	tgc
Arg	Gln	Lys	Val	Asn	Gly	Asp	Cys	Gln	Asn	Arg	Ser	Val	Cys	Ser	Cys
415					420					425					430
att	gtc	cag	cca	gtt	gaa	gaa	tct	gat	aac	gtg	aca	cag	gat	atg	aaa
Ile	Val	Gln	Pro	Val	Glu	Glu	Ser	Asp	Asn	Val	Thr	Gln	Asp	Met	Lys
				435					440					445	
gaa	act	gga	cca	gtt	acg	agc	aga	gaa	tat	gag	gag	aac	ggg	caa	ata
Glu	Thr	Gly	Pro	Val	Thr	Ser	Arg	Glu	Tyr	Glu	Glu	Asn	Gly	Gln	Ile
			450					455					460		
caa	cat	ggt	aaa	tca	agt	gat	ccc	aaa	ttc	tat	tct	tcg	gtg	tac	cca
Gln	His	Gly	Lys	Ser	Ser	Asp	Pro	Lys	Phe	Tyr	Ser	Ser	Val	Tyr	Pro
		465					470					475			
gag	tat	tgg	gtt	cct	gtg	cag	cta	tca	gat	gta	cag	ctg	gag	caa	tac
Glu	Tyr	Trp	Val	Pro	Val	Gln	Leu	Ser	Asp	Val	Gln	Leu	Glu	Gln	Tyr
	480					485					490				
tgt	cag	act	ctc	ttc	tcc	aaa	tcc	tta	tct	ctt	tct	tca	ctt	tcg	aag
Cys	Gln	Thr	Leu	Phe	Ser	Lys	Ser	Leu	Ser	Leu	Ser	Ser	Leu	Ser	Lys
495					500					505					510
att	gat	ctt	gga	gct	cta	gaa	gaa	act	ctc	aat	tct	gta	aga	aaa	acc
Ile	Asp	Leu	Gly	Ala	Leu	Glu	Glu	Thr	Leu	Asn	Ser	Val	Arg	Lys	Thr
				515					520					525	
tgt	gac	cat	cca	tac	gtt	atg	gat	gca	tct	ttg	aaa	caa	ctg	ctc	acc
Cys	Asp	His	Pro	Tyr	Val	Met	Asp	Ala	Ser	Leu	Lys	Gln	Leu	Leu	Thr
			530					535					540		
aag	aat	ctg	gag	ttg	cat	gaa	atc	ctg	gat	gta	gaa	att	aaa	gcg	agc
Lys	Asn	Leu	Glu	Leu	His	Glu	Ile	Leu	Asp	Val	Glu	Ile	Lys	Ala	Ser
		545					550					555			
ggg	aaa	ctt	cac	ctc	ctt	gat	aaa	atg	ctt	act	cat	ata	aaa	aag	aat
Gly	Lys	Leu	His	Leu	Leu	Asp	Lys	Met	Leu	Thr	His	Ile	Lys	Lys	Asn
	560					565					570				
ggt	tta	aaa	gca	gtt	gtc	ttc	tac	cag	gca	aca	caa	acc	cct	gaa	ggg
Gly	Leu	Lys	Ala	Val	Val	Phe	Tyr	Gln	Ala	Thr	Gln	Thr	Pro	Glu	Gly
575					580				585						590
ctt	ctg	ctt	ggt	aat	att	ctc	gaa	gat	ttt	gtg	ggt	caa	aga	ttt	ggt
Leu	Leu	Leu	Gly	Asn	Ile	Leu	Glu	Asp	Phe	Val	Gly	Gln	Arg	Phe	Gly
				595					600					605	
cca	aaa	tct	tat	gag	cat	ggg	ata	tat	tcc	tca	aag	aag	aac	tcc	gct
Pro	Lys	Ser	Tyr	Glu	His	Gly	Ile	Tyr	Ser	Ser	Lys	Lys	Asn	Ser	Ala
			610					615					620		
ata	aac	aat	ttc	aac	aag	gag	agt	caa	tgc	tgt	gtt	ctg	ctg	ttg	gaa
Ile	Asn	Asn	Phe	Asn	Lys	Glu	Ser	Gln	Cys	Cys	Val	Leu	Leu	Leu	Glu
		625					630					635			

Second Corrected Sequence Listing 5-2002																
aca	cgt	gcc	tgc	agt	caa	acc	att	aaa	ctc	ttg	cga	gct	gat	gcg	ttt	2271
Thr	Arg	Ala	Cys	Ser	Gln	Thr	Ile	Lys	Leu	Leu	Arg	Ala	Asp	Ala	Phe	
640						645					650					
att	ctt	ttt	gga	agc	agc	ttg	aat	cca	tcg	cat	gat	ggt	aag	cac	gta	2319
Ile	Leu	Phe	Gly	Ser	Ser	Leu	Asn	Pro	Ser	His	Asp	Val	Lys	His	Val	
655					660					665					670	
gag	aag	ata	aaa	atc	gag	tca	tgt	tct	gaa	aga	act	aag	ata	ttc	cga	2367
Glu	Lys	Ile	Lys	Ile	Glu	Ser	Cys	Ser	Glu	Arg	Thr	Lys	Ile	Phe	Arg	
				675					680					685		
ttg	tac	tca	gta	tgt	aca	gtt	gaa	gaa	aaa	gcc	ctg	att	ctg	gct	agg	2415
Leu	Tyr	Ser	Val	Cys	Thr	Val	Glu	Glu	Lys	Ala	Leu	Ile	Leu	Ala	Arg	
			690					695					700			
caa	aat	atg	cgg	caa	aat	aaa	gct	gta	gag	aac	cta	aac	cgc	tct	ctc	2463
Gln	Asn	Met	Arg	Gln	Asn	Lys	Ala	Val	Glu	Asn	Leu	Asn	Arg	Ser	Leu	
		705					710					715				
acg	cac	gca	ctg	ctc	atg	tgg	ggg	gcg	tca	tac	tta	ttt	gat	aaa	ctg	2511
Thr	His	Ala	Leu	Leu	Met	Trp	Gly	Ala	Ser	Tyr	Leu	Phe	Asp	Lys	Leu	
	720					725					730					
gat	cat	ttt	cac	agc	agt	gaa	act	cca	gat	tca	gga	ggt	tca	ttt	gaa	2559
Asp	His	Phe	His	Ser	Ser	Glu	Thr	Pro	Asp	Ser	Gly	Val	Ser	Phe	Glu	
735					740				745						750	
caa	tct	att	atg	gac	ggc	gtg	att	cat	gaa	ttc	tcg	tcc	ata	ctt	tct	2607
Gln	Ser	Ile	Met	Asp	Gly	Val	Ile	His	Glu	Phe	Ser	Ser	Ile	Leu	Ser	
				755					760					765		
tcc	aaa	ggt	gga	gaa	gaa	aat	gaa	gtc	aag	ctg	tgt	cta	ctt	ttg	gag	2655
Ser	Lys	Gly	Gly	Glu	Glu	Asn	Glu	Val	Lys	Leu	Cys	Leu	Leu	Leu	Glu	
			770					775					780			
gcc	aag	cat	gct	cag	gga	act	tac	agc	agt	gat	tct	act	cta	ttt	ggt	2703
Ala	Lys	His	Ala	Gln	Gly	Thr	Tyr	Ser	Ser	Asp	Ser	Thr	Leu	Phe	Gly	
		785					790					795				
gaa	gac	cat	att	aag	ttg	tca	gat	gaa	gag	agt	cca	aat	ata	ttt	tgg	2751
Glu	Asp	His	Ile	Lys	Leu	Ser	Asp	Glu	Glu	Ser	Pro	Asn	Ile	Phe	Trp	
	800					805					810					
tca	aag	ctg	ttg	ggg	gga	aaa	aat	cct	atg	tgg	aaa	tac	cct	tca	gat	2799
Ser	Lys	Leu	Leu	Gly	Gly	Lys	Asn	Pro	Met	Trp	Lys	Tyr	Pro	Ser	Asp	
815				820						825					830	
act	ccc	caa	agg	aat	cga	aaa	cga	gtt	cag	tat	ttt	gag	ggt	tct	gaa	2847
Thr	Pro	Gln	Arg	Asn	Arg	Lys	Arg	Val	Gln	Tyr	Phe	Glu	Gly	Ser	Glu	
				835					840					845		
gcg	agt	ccc	aaa	act	ggc	gat	ggt	gga	aat	gca	aag	aag	cga	aag	aag	2895
Ala	Ser	Pro	Lys	Thr	Gly	Asp	Gly	Gly	Asn	Ala	Lys	Lys	Arg	Lys	Lys	
			850					855					860			
gct	tct	gat	gat	gtc	act	gat	ccc	cgg	gtc	act	gat	ccg	cca	gta	gat	2943
Ala	Ser	Asp	Asp	Val	Thr	Asp	Pro	Arg	Val	Thr	Asp	Pro	Pro	Val	Asp	
		865					870					875				
gat	gat	gaa	aga	aag	gcc	tct	ggg	aag	gat	cac	atg	ggg	gct	ttg	gag	2991
Asp	Asp	Glu	Arg	Lys	Ala	Ser	Gly	Lys	Asp	His	Met	Gly	Ala	Leu	Glu	
	880					885					890					

Second Corrected Sequence Listing 5-2002

tca cca aaa gtc ata aca ctc cag tca tca tgt aaa tct tct ggt aca	3039
Ser Pro Lys Val Ile Thr Leu Gln Ser Ser Cys Lys Ser Ser Gly Thr	
895 900 905 910	
gat ggt aca ttg gat gga aat gat gct ttt ggc ttg tat tct atg ggc	3087
Asp Gly Thr Leu Asp Gly Asn Asp Ala Phe Gly Leu Tyr Ser Met Gly	
915 920 925	
agc cat atc tct gga atc cca gag gat atg tta gct agt caa gat tgg	3135
Ser His Ile Ser Gly Ile Pro Glu Asp Met Leu Ala Ser Gln Asp Trp	
930 935 940	
ggg aaa ata ccg gat gaa tca cag agg agg ctc cac act gtt tta aag	3183
Gly Lys Ile Pro Asp Glu Ser Gln Arg Arg Leu His Thr Val Leu Lys	
945 950 955	
ccg aag atg gca aaa ctt tgc caa gtt ttg cat ctt tca gat gct tgc	3231
Pro Lys Met Ala Lys Leu Cys Gln Val Leu His Leu Ser Asp Ala Cys	
960 965 970	
aca agc atg gtc gga aat ttt ctc gaa tat gtt att gaa aat cac cga	3279
Thr Ser Met Val Gly Asn Phe Leu Glu Tyr Val Ile Glu Asn His Arg	
975 980 985 990	
atc tac gaa gag cca gcc act act ttt cag gca ttc cag ata gcc ctg	3327
Ile Tyr Glu Glu Pro Ala Thr Thr Phe Gln Ala Phe Gln Ile Ala Leu	
995 1000 1005	
agt tgg att gca gcc ttg ttg gta aag caa att ctt agc cac aaa gaa	3375
Ser Trp Ile Ala Ala Leu Leu Val Lys Gln Ile Leu Ser His Lys Glu	
1010 1015 1020	
tct ctg gtc cgt gca aat tct gaa tta gct ttc aaa tgc tct aga gta	3423
Ser Leu Val Arg Ala Asn Ser Glu Leu Ala Phe Lys Cys Ser Arg Val	
1025 1030 1035	
gag gtg gat tat att tat tcg ata ttg tcc tgc atg aag agt ctg ttc	3471
Glu Val Asp Tyr Ile Tyr Ser Ile Leu Ser Cys Met Lys Ser Leu Phe	
1040 1045 1050	
ctg gag cat aca caa ggt ttg cag ttc gat tgc ttt ggt act aat tct	3519
Leu Glu His Thr Gln Gly Leu Gln Phe Asp Cys Phe Gly Thr Asn Ser	
1055 1060 1065 1070	
aaa cag tca gtg gtt agc aca aaa cta gta aat gaa agt ctc tca ggg	3567
Lys Gln Ser Val Val Ser Thr Lys Leu Val Asn Glu Ser Leu Ser Gly	
1075 1080 1085	
gct aca gtg cgt gac gaa aag att aat acg aag tcg atg cga aat agc	3615
Ala Thr Val Arg Asp Glu Lys Ile Asn Thr Lys Ser Met Arg Asn Ser	
1090 1095 1100	
tca gag gat gaa gag tgc atg act gag aag aga tgt agc cat tat agc	3663
Ser Glu Asp Glu Glu Cys Met Thr Glu Lys Arg Cys Ser His Tyr Ser	
1105 1110 1115	
aca gca aca aga gat atc gaa aag act att agt ggc ata aaa aag aaa	3711
Thr Ala Thr Arg Asp Ile Glu Lys Thr Ile Ser Gly Ile Lys Lys Lys	
1120 1125 1130	
tac aag aag caa gtg caa aag ctt gta caa gag cat gag gaa aag aaa	3759
Tyr Lys Lys Gln Val Gln Lys Leu Val Gln Glu His Glu Glu Lys Lys	

Second Corrected Sequence Listing 5-2002

1135	1140	1145	1150	
atg gag ctg tta aat atg tat gca gac aag aag cag aaa ctt gaa act				3807
Met Glu Leu Leu Asn Met Tyr Ala Asp Lys Lys Gln Lys Leu Glu Thr	1155	1160	1165	
agt aaa agt gtg gaa gca gca gta att cgt att acc tgt tca cgg acc				3855
Ser Lys Ser Val Glu Ala Ala Val Ile Arg Ile Thr Cys Ser Arg Thr	1170	1175	1180	
agt act caa gtg ggt gat ctc aaa ctg ctg gat cat aat tat gaa aga				3903
Ser Thr Gln Val Gly Asp Leu Lys Leu Leu Asp His Asn Tyr Glu Arg	1185	1190	1195	
aag ttt gat gaa atc aaa agt gag aaa aat gaa tgc ctc aaa agt ctg				3951
Lys Phe Asp Glu Ile Lys Ser Glu Lys Asn Glu Cys Leu Lys Ser Leu	1200	1205	1210	
gag caa atg cac gag gtt gca aag aag aag ttg gct gag gat gaa gcc				3999
Glu Gln Met His Glu Val Ala Lys Lys Lys Leu Ala Glu Asp Glu Ala	1215	1220	1225	1230
tgt tgg att aat cgg ata aag agc tgg gca gct aaa tta aaa gtt tgt				4047
Cys Trp Ile Asn Arg Ile Lys Ser Trp Ala Ala Lys Leu Lys Val Cys	1235	1240	1245	
gtt ccc att caa agt ggc aat aac aag cat ttt agt ggt tca tca aac				4095
Val Pro Ile Gln Ser Gly Asn Asn Lys His Phe Ser Gly Ser Ser Asn	1250	1255	1260	
att tcc caa aat gct cct gat gta caa att tgc aat aat gct aac gtt				4143
Ile Ser Gln Asn Ala Pro Asp Val Gln Ile Cys Asn Asn Ala Asn Val	1265	1270	1275	
gaa gct act tac gct gat acg aat tgc atg gct tcc aag gtt aat caa				4191
Glu Ala Thr Tyr Ala Asp Thr Asn Cys Met Ala Ser Lys Val Asn Gln	1280	1285	1290	
gtg cca gaa gca gaa aac aca tta gga acc atg tgc ggt ggc agc act				4239
Val Pro Glu Ala Glu Asn Thr Leu Gly Thr Met Ser Gly Gly Ser Thr	1295	1300	1305	1310
caa caa gtt cat gaa atg gtg gat gta aga aat gac gag aca atg gat				4287
Gln Gln Val His Glu Met Val Asp Val Arg Asn Asp Glu Thr Met Asp	1315	1320	1325	
gtc tca gct ttg tct cgt gaa cag ctt aca aag agc cag tcc aat gag				4335
Val Ser Ala Leu Ser Arg Glu Gln Leu Thr Lys Ser Gln Ser Asn Glu	1330	1335	1340	
cac gct tct atc act gtg cct gag att ttg att cct gct gac tgt caa				4383
His Ala Ser Ile Thr Val Pro Glu Ile Leu Ile Pro Ala Asp Cys Gln	1345	1350	1355	
gag gaa ttt gcg gcc ttg aac gtg cat ttg tca gaa gac cag aat tgt				4431
Glu Glu Phe Ala Ala Leu Asn Val His Leu Ser Glu Asp Gln Asn Cys	1360	1365	1370	
gac aga ata aca tct gcg gca tca gat gaa gat gtt tca tca agg gtg				4479
Asp Arg Ile Thr Ser Ala Ala Ser Asp Glu Asp Val Ser Ser Arg Val	1375	1380	1385	1390
cca gag gta tcc cag tca ctc gaa aat ctt tct gcc tcc ccc gag ttt				4527

Second Corrected Sequence Listing 5-2002

Pro	Glu	Val	Ser	Gln	Ser	Leu	Glu	Asn	Leu	Ser	Ala	Ser	Pro	Glu	Phe	
				1395					1400						1405	
tct	cta	aat	aga	gag	gag	gct	ttg	gtt	aca	aca	gaa	aat	aga	aga	aca	4575
Ser	Leu	Asn	Arg	Glu	Glu	Ala	Leu	Val	Thr	Thr	Glu	Asn	Arg	Arg	Thr	
			1410					1415					1420			
agt	cat	gtg	ggg	ttt	gat	act	gat	aac	att	ttg	gac	cag	cag	aat	aga	4623
Ser	His	Val	Gly	Phe	Asp	Thr	Asp	Asn	Ile	Leu	Asp	Gln	Gln	Asn	Arg	
		1425					1430					1435				
gaa	gat	tgt	tct	ctt	gac	caa	gag	att	cct	gac	gag	tta	gcg	atg	cct	4671
Glu	Asp	Cys	Ser	Leu	Asp	Gln	Glu	Ile	Pro	Asp	Glu	Leu	Ala	Met	Pro	
	1440					1445					1450					
gtg	caa	cat	ctt	gcg	tct	gtg	gta	gag	act	agg	ggg	gct	gct	gaa	tct	4719
Val	Gln	His	Leu	Ala	Ser	Val	Val	Glu	Thr	Arg	Gly	Ala	Ala	Glu	Ser	
	1455					1460				1465					1470	
gat	cag	tat	ggg	caa	gat	ata	tgt	cct	atg	cct	tct	tca	ctg	gct	gga	4767
Asp	Gln	Tyr	Gly	Gln	Asp	Ile	Cys	Pro	Met	Pro	Ser	Ser	Leu	Ala	Gly	
			1475						1480					1485		
aag	caa	cct	gac	cca	gca	gca	aac	act	gag	agc	gaa	aat	ctt	gaa	gaa	4815
Lys	Gln	Pro	Asp	Pro	Ala	Ala	Asn	Thr	Glu	Ser	Glu	Asn	Leu	Glu	Glu	
			1490					1495					1500			
gca	att	gag	cct	cag	tct	gct	ggg	tca	gaa	aca	gta	gag	act	act	gat	4863
Ala	Ile	Glu	Pro	Gln	Ser	Ala	Gly	Ser	Glu	Thr	Val	Glu	Thr	Thr	Asp	
		1505					1510					1515				
ttt	gct	gca	tca	cat	cag	ggg	gat	caa	gtt	aca	tgt	cct	ttg	cta	tct	4911
Phe	Ala	Ala	Ser	His	Gln	Gly	Asp	Gln	Val	Thr	Cys	Pro	Leu	Leu	Ser	
	1520					1525					1530					
tca	ccg	act	gga	aat	cag	cct	gcg	cca	gaa	gca	aat	att	gaa	ggc	caa	4959
Ser	Pro	Thr	Gly	Asn	Gln	Pro	Ala	Pro	Glu	Ala	Asn	Ile	Glu	Gly	Gln	
	1535				1540					1545				1550		
aat	atc	aac	aca	tca	gct	gag	ccc	cat	gta	gcg	ggg	cca	gat	gca	gta	5007
Asn	Ile	Asn	Thr	Ser	Ala	Glu	Pro	His	Val	Ala	Gly	Pro	Asp	Ala	Val	
				1555					1560					1565		
gag	agt	ggg	gat	tat	gca	gta	ata	gat	cag	gaa	aca	atg	ggg	gct	cag	5055
Glu	Ser	Gly	Asp	Tyr	Ala	Val	Ile	Asp	Gln	Glu	Thr	Met	Gly	Ala	Gln	
		1570						1575					1580			
gat	gca	tgc	tct	ctg	cca	tct	gga	tcg	gtt	gga	act	cag	tct	gac	cta	5103
Asp	Ala	Cys	Ser	Leu	Pro	Ser	Gly	Ser	Val	Gly	Thr	Gln	Ser	Asp	Leu	
		1585					1590					1595				
gga	gca	aac	att	gag	ggg	caa	aat	gtc	aca	aca	gtg	gct	caa	ctt	ccc	5151
Gly	Ala	Asn	Ile	Glu	Gly	Gln	Asn	Val	Thr	Thr	Val	Ala	Gln	Leu	Pro	
	1600					1605					1610					
aca	gat	gga	tca	gat	gca	gtt	gta	acc	ggg	gga	tct	cct	gta	tca	gat	5199
Thr	Asp	Gly	Ser	Asp	Ala	Val	Val	Thr	Gly	Gly	Ser	Pro	Val	Ser	Asp	
	1615				1620					1625					1630	
cag	tgt	gcc	cag	gat	gca	tct	cct	atg	cca	tta	tct	tcg	cct	gga	aat	5247
Gln	Cys	Ala	Gln	Asp	Ala	Ser	Pro	Met	Pro	Leu	Ser	Ser	Pro	Gly	Asn	
				1635					1640					1645		

Second Corrected Sequence Listing 5-2002

cac cct gat aca gca gtt aat atc gag ggt tta gat aac aca tca gta His Pro Asp Thr Ala Val Asn Ile Glu Gly Leu Asp Asn Thr Ser Val 1650 1655 1660	5295
gct gag cct cat ata agt gga tca gat gca tgt gaa atg gaa att tca Ala Glu Pro His Ile Ser Gly Ser Asp Ala Cys Glu Met Glu Ile Ser 1665 1670 1675	5343
gaa cct ggt ccc caa gta gag cgg tca acc ttt gca aat ctt ttc cat Glu Pro Gly Pro Gln Val Glu Arg Ser Thr Phe Ala Asn Leu Phe His 1680 1685 1690	5391
gaa ggt ggc gtg gag cat tca gca ggt gta aca gct ctt gtt cca tca Glu Gly Gly Val Glu His Ser Ala Gly Val Thr Ala Leu Val Pro Ser 1695 1700 1705 1710	5439
ctt ctt aac aat ggt acg gaa cag att gcc gtt caa cct gtt cct caa Leu Leu Asn Asn Gly Thr Glu Gln Ile Ala Val Gln Pro Val Pro Gln 1715 1720 1725	5487
ata cct ttc cct gtg ttc aac gac ccg ttt ctg cat gaa ctg gag aag Ile Pro Phe Pro Val Phe Asn Asp Pro Phe Leu His Glu Leu Glu Lys 1730 1735 1740	5535
ttg cgg aga gaa tca gag aac tca aag aag act ttt gaa gaa aaa aaa Leu Arg Arg Glu Ser Glu Asn Ser Lys Lys Thr Phe Glu Glu Lys Lys 1745 1750 1755	5583
tca atc ttg aaa gct gaa ctc gag agg aag atg gct gaa gta caa gca Ser Ile Leu Lys Ala Glu Leu Glu Arg Lys Met Ala Glu Val Gln Ala 1760 1765 1770	5631
gag ttt cga aga aaa ttt cat gag gta gaa gcc gag cat aac acc aga Glu Phe Arg Arg Lys Phe His Glu Val Glu Ala Glu His Asn Thr Arg 1775 1780 1785 1790	5679
acg aca aag ata gag aag gat aag aat ctt gtt ata atg aac aaa ctg Thr Thr Lys Ile Glu Lys Asp Lys Asn Leu Val Ile Met Asn Lys Leu 1795 1800 1805	5727
ttg gcg aat gcg ttc ttg tcc aaa tgt act gac aag aag gta tct ccc Leu Ala Asn Ala Phe Leu Ser Lys Cys Thr Asp Lys Lys Val Ser Pro 1810 1815 1820	5775
tca gga gct cca agg ggt aaa att cag cag cta gca cag aga gca gca Ser Gly Ala Pro Arg Gly Lys Ile Gln Gln Leu Ala Gln Arg Ala Ala 1825 1830 1835	5823
caa gtg agt gca ctg aga aat tac att gct cct cag cag ctt cag gca Gln Val Ser Ala Leu Arg Asn Tyr Ile Ala Pro Gln Gln Leu Gln Ala 1840 1845 1850	5871
tct tct ttt cct gct cct gct ctg gtt tcg gct cct ctg caa ctt cag Ser Ser Phe Pro Ala Pro Ala Leu Val Ser Ala Pro Leu Gln Leu Gln 1855 1860 1865 1870	5919
caa tca tca ttt cct gct cct ggt ccg gct cct ctg cag cct cag gca Gln Ser Ser Phe Pro Ala Pro Gly Pro Ala Pro Leu Gln Pro Gln Ala 1875 1880 1885	5967
tct tcg ttt cct tct tca gtc tct cgt cca tca gcc ctt ctt ctg aat Ser Ser Phe Pro Ser Ser Val Ser Arg Pro Ser Ala Leu Leu Leu Asn 1890 1895 1900	6015

Second Corrected Sequence Listing 5-2002

ttt gcg gtc tgt cca atg cct cag ccc aga cag cct ctc ata tcc aac	6063
Phe Ala Val Cys Pro Met Pro Gln Pro Arg Gln Pro Leu Ile Ser Asn	
1905 1910 1915	
ata gct cca act cca tca gtt act cct gca aca aat cca ggt ctg cgt	6111
Ile Ala Pro Thr Pro Ser Val Thr Pro Ala Thr Asn Pro Gly Leu Arg	
1920 1925 1930	
tct cct gca cca cac cta aac tca tat aga cca tcc tct tca act ccc	6159
Ser Pro Ala Pro His Leu Asn Ser Tyr Arg Pro Ser Ser Ser Thr Pro	
1935 1940 1945 1950	
gtc gcc aca gct act cca acc tcg tca gtg cct cct caa gct ttg aca	6207
Val Ala Thr Ala Thr Pro Thr Ser Ser Val Pro Pro Gln Ala Leu Thr	
1955 1960 1965	
tat tca gct gtg tca att cag cag cag caa gaa caa caa ccg caa cag	6255
Tyr Ser Ala Val Ser Ile Gln Gln Gln Gln Glu Gln Gln Pro Gln Gln	
1970 1975 1980	
agc ttg agc agt gga ttg cag agc aac aat gaa gtg gtt tgt ctt tct	6303
Ser Leu Ser Ser Gly Leu Gln Ser Asn Asn Glu Val Val Cys Leu Ser	
1985 1990 1995	
gac gac gag tgacctaaga ggagagatgg ttagggctctt agttattgat	6352
Asp Asp Glu	
2000	
tttttagagag ttaataatag tatatatata tatgtataag taggttacct aatctctgtc	6412
gttaatctaa tttagtgagt caggaaccga ctcgttggct aaggctctctc cttttgaaac	6472
gcaacgttct actttcatgt atataaatac agtctgatca cacaacacaa attgatgatt	6532
gaaaatacta ctgattttaac ttaaaaaaaaa aaaaaaaaaa	6571

<210> 3
 <211> 2001
 <212> PRT
 <213> Arabidopsis thaliana

<400> 3
 Met Lys Lys Asp Glu Lys Ile Gly Leu Thr Gly Arg Thr Ile Tyr Thr
 1 5 10 15
 Arg Ser Leu Ala Ala Ser Ile Pro Ala Ser Val Glu Gln Glu Thr Pro
 20 25 30
 Gly Leu Arg Arg Ser Ser Arg Gly Thr Pro Ser Thr Lys Val Ile Thr
 35 40 45
 Pro Ala Ser Ala Thr Arg Lys Ser Glu Arg Leu Ala Pro Ser Pro Ala
 50 55 60
 Ser Val Ser Lys Lys Ser Gly Gly Ile Val Lys Asn Ser Thr Pro Ser
 65 70 75 80
 Ser Leu Arg Arg Ser Asn Arg Gly Lys Thr Glu Val Ser Leu Gln Ser
 85 90 95
 Ser Lys Gly Ser Asp Asn Ser Ile Arg Lys Gly Asp Thr Ser Pro Asp

Second Corrected Sequence Listing 5-2002

100																			
Ile	Glu	Gln	Arg	Lys	Asp	Ser	Val	Glu	Glu	Ser	Thr	Asp	Lys	Ile	Lys				
		115					120					125							
Pro	Ile	Met	Ser	Ala	Arg	Ser	Tyr	Arg	Ala	Leu	Phe	Arg	Gly	Lys	Leu				
	130					135					140								
Lys	Glu	Ser	Glu	Ala	Leu	Val	Asp	Ala	Ser	Pro	Asn	Glu	Glu	Glu	Leu				
145					150					155					160				
Val	Val	Val	Gly	Cys	Ser	Arg	Arg	Ile	Pro	Ala	Gly	Asn	Asp	Asp	Val				
				165					170					175					
Gln	Gly	Lys	Thr	Asp	Cys	Pro	Pro	Pro	Ala	Asp	Ala	Gly	Ser	Lys	Arg				
			180					185					190						
Leu	Pro	Val	Asp	Glu	Thr	Ser	Leu	Asp	Lys	Gly	Thr	Asp	Phe	Pro	Leu				
		195					200					205							
Lys	Ser	Val	Thr	Glu	Thr	Glu	Lys	Ile	Val	Leu	Asp	Ala	Ser	Pro	Ile				
	210					215					220								
Val	Glu	Thr	Gly	Asp	Asp	Ser	Val	Ile	Gly	Ser	Pro	Ser	Glu	Asn	Leu				
225					230					235					240				
Glu	Thr	Gln	Lys	Leu	Gln	Asp	Gly	Lys	Thr	Asp	Cys	Ser	Pro	Pro	Ala				
				245					250					255					
Asn	Ala	Glu	Ser	Lys	Thr	Leu	Pro	Val	Gly	Glu	Thr	Ser	Leu	Glu	Lys				
			260					265					270						
Glu	Tyr	Pro	Gln	Lys	Phe	Gln	Asp	Asp	Asn	Thr	Asp	Cys	Leu	Pro	Pro				
		275					280					285							
Ala	Asn	Ala	Glu	Ser	Lys	Arg	Leu	Pro	Val	Gly	Glu	Thr	Ser	Leu	Glu				
	290					295					300								
Lys	Asp	Thr	Asp	Phe	Pro	Leu	Lys	Ser	Thr	Thr	Glu	Thr	Gly	Lys	Met				
305					310					315					320				
Val	Leu	Tyr	Ala	Ser	Pro	Ile	Val	Glu	Thr	Arg	Asp	Asp	Ser	Val	Ile				
				325					330					335					
Cys	Ser	Pro	Ser	Thr	Asn	Leu	Glu	Thr	Gln	Lys	Leu	Leu	Val	Ser	Lys				
			340					345					350						
Thr	Gly	Leu	Glu	Thr	Asp	Ile	Val	Leu	Pro	Leu	Lys	Arg	Lys	Arg	Asp				
		355					360					365							
Thr	Ala	Glu	Ile	Glu	Leu	Asp	Ala	Cys	Ala	Thr	Val	Ala	Asn	Gly	Asp				
	370					375					380								
Asp	His	Val	Met	Ser	Ser	Asp	Gly	Val	Ile	Pro	Ser	Pro	Ser	Gly	Cys				
385					390					395					400				
Lys	Asn	Asp	Asn	Arg	Pro	Glu	Met	Cys	Asn	Thr	Cys	Lys	Lys	Arg	Gln				
				405					410					415					
Lys	Val	Asn	Gly	Asp	Cys	Gln	Asn	Arg	Ser	Val	Cys	Ser	Cys	Ile	Val				
			420					425					430						
Gln	Pro	Val	Glu	Glu	Ser	Asp	Asn	Val	Thr	Gln	Asp	Met	Lys	Glu	Thr				

Second Corrected Sequence Listing 5-2002

435

440

445

Gly	Pro	Val	Thr	Ser	Arg	Glu	Tyr	Glu	Glu	Asn	Gly	Gln	Ile	Gln	His
450						455					460				
Gly	Lys	Ser	Ser	Asp	Pro	Lys	Phe	Tyr	Ser	Ser	Val	Tyr	Pro	Glu	Tyr
465					470					475					480
Trp	Val	Pro	Val	Gln	Leu	Ser	Asp	Val	Gln	Leu	Glu	Gln	Tyr	Cys	Gln
				485					490					495	
Thr	Leu	Phe	Ser	Lys	Ser	Leu	Ser	Leu	Ser	Ser	Leu	Ser	Lys	Ile	Asp
			500					505					510		
Leu	Gly	Ala	Leu	Glu	Glu	Thr	Leu	Asn	Ser	Val	Arg	Lys	Thr	Cys	Asp
		515					520					525			
His	Pro	Tyr	Val	Met	Asp	Ala	Ser	Leu	Lys	Gln	Leu	Leu	Thr	Lys	Asn
	530					535					540				
Leu	Glu	Leu	His	Glu	Ile	Leu	Asp	Val	Glu	Ile	Lys	Ala	Ser	Gly	Lys
545					550					555					560
Leu	His	Leu	Leu	Asp	Lys	Met	Leu	Thr	His	Ile	Lys	Lys	Asn	Gly	Leu
				565					570					575	
Lys	Ala	Val	Val	Phe	Tyr	Gln	Ala	Thr	Gln	Thr	Pro	Glu	Gly	Leu	Leu
			580					585					590		
Leu	Gly	Asn	Ile	Leu	Glu	Asp	Phe	Val	Gly	Gln	Arg	Phe	Gly	Pro	Lys
		595					600					605			
Ser	Tyr	Glu	His	Gly	Ile	Tyr	Ser	Ser	Lys	Lys	Asn	Ser	Ala	Ile	Asn
	610					615					620				
Asn	Phe	Asn	Lys	Glu	Ser	Gln	Cys	Cys	Val	Leu	Leu	Leu	Glu	Thr	Arg
625					630					635					640
Ala	Cys	Ser	Gln	Thr	Ile	Lys	Leu	Leu	Arg	Ala	Asp	Ala	Phe	Ile	Leu
				645					650					655	
Phe	Gly	Ser	Ser	Leu	Asn	Pro	Ser	His	Asp	Val	Lys	His	Val	Glu	Lys
			660					665					670		
Ile	Lys	Ile	Glu	Ser	Cys	Ser	Glu	Arg	Thr	Lys	Ile	Phe	Arg	Leu	Tyr
		675					680					685			
Ser	Val	Cys	Thr	Val	Glu	Glu	Lys	Ala	Leu	Ile	Leu	Ala	Arg	Gln	Asn
	690					695					700				
Met	Arg	Gln	Asn	Lys	Ala	Val	Glu	Asn	Leu	Asn	Arg	Ser	Leu	Thr	His
705					710					715					720
Ala	Leu	Leu	Met	Trp	Gly	Ala	Ser	Tyr	Leu	Phe	Asp	Lys	Leu	Asp	His
				725					730					735	
Phe	His	Ser	Ser	Glu	Thr	Pro	Asp	Ser	Gly	Val	Ser	Phe	Glu	Gln	Ser
			740					745					750		
Ile	Met	Asp	Gly	Val	Ile	His	Glu	Phe	Ser	Ser	Ile	Leu	Ser	Ser	Lys
		755					760					765			
Gly	Gly	Glu	Glu	Asn	Glu	Val	Lys	Leu	Cys	Leu	Leu	Leu	Glu	Ala	Lys

Second Corrected Sequence Listing 5-2002

770

775

780

His Ala Gln Gly Thr Tyr Ser Ser Asp Ser Thr Leu Phe Gly Glu Asp
785 790 795 800
His Ile Lys Leu Ser Asp Glu Glu Ser Pro Asn Ile Phe Trp Ser Lys
805 810 815
Leu Leu Gly Gly Lys Asn Pro Met Trp Lys Tyr Pro Ser Asp Thr Pro
820 825 830
Gln Arg Asn Arg Lys Arg Val Gln Tyr Phe Glu Gly Ser Glu Ala Ser
835 840 845
Pro Lys Thr Gly Asp Gly Gly Asn Ala Lys Lys Arg Lys Lys Ala Ser
850 855 860
Asp Asp Val Thr Asp Pro Arg Val Thr Asp Pro Pro Val Asp Asp Asp
865 870 875 880
Glu Arg Lys Ala Ser Gly Lys Asp His Met Gly Ala Leu Glu Ser Pro
885 890 895
Lys Val Ile Thr Leu Gln Ser Ser Cys Lys Ser Ser Gly Thr Asp Gly
900 905 910
Thr Leu Asp Gly Asn Asp Ala Phe Gly Leu Tyr Ser Met Gly Ser His
915 920 925
Ile Ser Gly Ile Pro Glu Asp Met Leu Ala Ser Gln Asp Trp Gly Lys
930 935 940
Ile Pro Asp Glu Ser Gln Arg Arg Leu His Thr Val Leu Lys Pro Lys
945 950 955 960
Met Ala Lys Leu Cys Gln Val Leu His Leu Ser Asp Ala Cys Thr Ser
965 970 975
Met Val Gly Asn Phe Leu Glu Tyr Val Ile Glu Asn His Arg Ile Tyr
980 985 990
Glu Glu Pro Ala Thr Thr Phe Gln Ala Phe Gln Ile Ala Leu Ser Trp
995 1000 1005
Ile Ala Ala Leu Leu Val Lys Gln Ile Leu Ser His Lys Glu Ser
1010 1015 1020
Leu Val Arg Ala Asn Ser Glu Leu Ala Phe Lys Cys Ser Arg Val
1025 1030 1035
Glu Val Asp Tyr Ile Tyr Ser Ile Leu Ser Cys Met Lys Ser Leu
1040 1045 1050
Phe Leu Glu His Thr Gln Gly Leu Gln Phe Asp Cys Phe Gly Thr
1055 1060 1065
Asn Ser Lys Gln Ser Val Val Ser Thr Lys Leu Val Asn Glu Ser
1070 1075 1080
Leu Ser Gly Ala Thr Val Arg Asp Glu Lys Ile Asn Thr Lys Ser
1085 1090 1095
Met Arg Asn Ser Ser Glu Asp Glu Glu Cys Met Thr Glu Lys Arg

Second Corrected Sequence Listing 5-2002

1100	1105	1110
Cys Ser His Tyr Ser Thr	Ala Thr Arg Asp Ile	Glu Lys Thr Ile
1115	1120	1125
Ser Gly Ile Lys Lys Lys	Tyr Lys Lys Gln Val	Gln Lys Leu Val
1130	1135	1140
Gln Glu His Glu Glu Lys	Lys Met Glu Leu Leu	Asn Met Tyr Ala
1145	1150	1155
Asp Lys Lys Gln Lys Leu	Glu Thr Ser Lys Ser	Val Glu Ala Ala
1160	1165	1170
Val Ile Arg Ile Thr Cys	Ser Arg Thr Ser Thr	Gln Val Gly Asp
1175	1180	1185
Leu Lys Leu Leu Asp His	Asn Tyr Glu Arg Lys	Phe Asp Glu Ile
1190	1195	1200
Lys Ser Glu Lys Asn Glu	Cys Leu Lys Ser Leu	Glu Gln Met His
1205	1210	1215
Glu Val Ala Lys Lys Lys	Leu Ala Glu Asp Glu	Ala Cys Trp Ile
1220	1225	1230
Asn Arg Ile Lys Ser Trp	Ala Ala Lys Leu Lys	Val Cys Val Pro
1235	1240	1245
Ile Gln Ser Gly Asn Asn	Lys His Phe Ser Gly	Ser Ser Asn Ile
1250	1255	1260
Ser Gln Asn Ala Pro Asp	Val Gln Ile Cys Asn	Asn Ala Asn Val
1265	1270	1275
Glu Ala Thr Tyr Ala Asp	Thr Asn Cys Met Ala	Ser Lys Val Asn
1280	1285	1290
Gln Val Pro Glu Ala Glu	Asn Thr Leu Gly Thr	Met Ser Gly Gly
1295	1300	1305
Ser Thr Gln Gln Val His	Glu Met Val Asp Val	Arg Asn Asp Glu
1310	1315	1320
Thr Met Asp Val Ser Ala	Leu Ser Arg Glu Gln	Leu Thr Lys Ser
1325	1330	1335
Gln Ser Asn Glu His Ala	Ser Ile Thr Val Pro	Glu Ile Leu Ile
1340	1345	1350
Pro Ala Asp Cys Gln Glu	Glu Phe Ala Ala Leu	Asn Val His Leu
1355	1360	1365
Ser Glu Asp Gln Asn Cys	Asp Arg Ile Thr Ser	Ala Ala Ser Asp
1370	1375	1380
Glu Asp Val Ser Ser Arg	Val Pro Glu Val Ser	Gln Ser Leu Glu
1385	1390	1395
Asn Leu Ser Ala Ser Pro	Glu Phe Ser Leu Asn	Arg Glu Glu Ala
1400	1405	1410
Leu Val Thr Thr Glu Asn	Arg Arg Thr Ser His	Val Gly Phe Asp

Second Corrected Sequence Listing 5-2002

1415	1420	1425
Thr Asp 1430 Asn Ile Leu Asp 1435 Gln 1435 Gln Asn Arg Glu 1440 Asp 1440 Cys Ser Leu		
Asp Gln 1445 Glu Ile Pro Asp 1450 Glu 1450 Leu Ala Met Pro Val 1455 Gln His Leu		
Ala Ser 1460 Val Val Glu Thr Arg 1465 Gly Ala Ala Glu Ser 1470 Asp Gln Tyr		
Gly Gln 1475 Asp Ile Cys Pro Met 1480 Pro Ser Ser Leu Ala 1485 Gly Lys Gln		
Pro Asp 1490 Pro Ala Ala Asn Thr 1495 Glu Ser Glu Asn Leu 1500 Glu Glu Ala		
Ile Glu 1505 Pro Gln Ser Ala Gly 1510 Ser Glu Thr Val Glu 1515 Thr Thr Asp		
Phe Ala 1520 Ala Ser His Gln Gly 1525 Asp Gln Val Thr Cys 1530 Pro Leu Leu		
Ser Ser 1535 Pro Thr Gly Asn Gln 1540 Pro Ala Pro Glu Ala 1545 Asn Ile Glu		
Gly Gln 1550 Asn Ile Asn Thr Ser 1555 Ala Glu Pro His Val 1560 Ala Gly Pro		
Asp Ala 1565 Val Glu Ser Gly Asp 1570 Tyr Ala Val Ile Asp 1575 Gln Glu Thr		
Met Gly 1580 Ala Gln Asp Ala Cys 1585 Ser Leu Pro Ser Gly 1590 Ser Val Gly		
Thr Gln 1595 Ser Asp Leu Gly Ala 1600 Asn Ile Glu Gly Gln 1605 Asn Val Thr		
Thr Val 1610 Ala Gln Leu Pro Thr 1615 Asp Gly Ser Asp Ala 1620 Val Val Thr		
Gly Gly 1625 Ser Pro Val Ser Asp 1630 Gln Cys Ala Gln Asp 1635 Ala Ser Pro		
Met Pro 1640 Leu Ser Ser Pro Gly 1645 Asn His Pro Asp Thr 1650 Ala Val Asn		
Ile Glu 1655 Gly Leu Asp Asn Thr 1660 Ser Val Ala Glu Pro 1665 His Ile Ser		
Gly Ser 1670 Asp Ala Cys Glu Met 1675 Glu Ile Ser Glu Pro 1680 Gly Pro Gln		
Val Glu 1685 Arg Ser Thr Phe Ala 1690 Asn Leu Phe His Glu 1695 Gly Gly Val		
Glu His 1700 Ser Ala Gly Val Thr 1705 Ala Leu Val Pro Ser 1710 Leu Leu Asn		
Asn Gly 1715 Thr Glu Gln Ile Ala 1720 Val Gln Pro Val Pro 1725 Gln Ile Pro		
Phe Pro Val Phe Asn Asp Pro Phe Leu His Glu Leu Glu Lys Leu		

Second Corrected Sequence Listing 5-2002

1730	1735	1740													
Arg	Arg	Glu	Ser	Glu	Asn	Ser	Lys	Lys	Thr	Phe	Glu	Glu	Lys	Lys	
1745						1750					1755				
Ser	Ile	Leu	Lys	Ala	Glu	Leu	Glu	Arg	Lys	Met	Ala	Glu	Val	Gln	
1760						1765					1770				
Ala	Glu	Phe	Arg	Arg	Lys	Phe	His	Glu	Val	Glu	Ala	Glu	His	Asn	
1775						1780					1785				
Thr	Arg	Thr	Thr	Lys	Ile	Glu	Lys	Asp	Lys	Asn	Leu	Val	Ile	Met	
1790						1795					1800				
Asn	Lys	Leu	Leu	Ala	Asn	Ala	Phe	Leu	Ser	Lys	Cys	Thr	Asp	Lys	
1805						1810					1815				
Lys	Val	Ser	Pro	Ser	Gly	Ala	Pro	Arg	Gly	Lys	Ile	Gln	Gln	Leu	
1820						1825					1830				
Ala	Gln	Arg	Ala	Ala	Gln	Val	Ser	Ala	Leu	Arg	Asn	Tyr	Ile	Ala	
1835						1840					1845				
Pro	Gln	Gln	Leu	Gln	Ala	Ser	Ser	Phe	Pro	Ala	Pro	Ala	Leu	Val	
1850						1855					1860				
Ser	Ala	Pro	Leu	Gln	Leu	Gln	Gln	Ser	Ser	Phe	Pro	Ala	Pro	Gly	
1865						1870					1875				
Pro	Ala	Pro	Leu	Gln	Pro	Gln	Ala	Ser	Ser	Phe	Pro	Ser	Ser	Val	
1880						1885					1890				
Ser	Arg	Pro	Ser	Ala	Leu	Leu	Leu	Asn	Phe	Ala	Val	Cys	Pro	Met	
1895						1900					1905				
Pro	Gln	Pro	Arg	Gln	Pro	Leu	Ile	Ser	Asn	Ile	Ala	Pro	Thr	Pro	
1910						1915					1920				
Ser	Val	Thr	Pro	Ala	Thr	Asn	Pro	Gly	Leu	Arg	Ser	Pro	Ala	Pro	
1925						1930					1935				
His	Leu	Asn	Ser	Tyr	Arg	Pro	Ser	Ser	Ser	Thr	Pro	Val	Ala	Thr	
1940						1945					1950				
Ala	Thr	Pro	Thr	Ser	Ser	Val	Pro	Pro	Gln	Ala	Leu	Thr	Tyr	Ser	
1955						1960					1965				
Ala	Val	Ser	Ile	Gln	Gln	Gln	Gln	Glu	Gln	Gln	Pro	Gln	Gln	Ser	
1970						1975					1980				
Leu	Ser	Ser	Gly	Leu	Gln	Ser	Asn	Asn	Glu	Val	Val	Cys	Leu	Ser	
1985						1990					1995				
Asp	Asp	Glu													

<210> 4
 <211> 21
 <212> DNA
 <213> Artificial Sequence

Second Corrected Sequence Listing 5-2002

<220>
 <223> Description of Artificial Sequence: Synthetic
 Oligonucleotide

 <400> 4
 catctacggc aatgtaccag c 21

 <210> 5
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 Oligonucleotide

 <400> 5
 gatgggaatt ggctgagtgg c 21

 <210> 6
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide

 <400> 6
 cagttcctaaa cgtaaacgg c 21

 <210> 7
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide
 n= a, t, g, or c; w= a or t

 <400> 7
 ntcgastwts gwggt 15

 <210> 8
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide
 n= a, t, g, or c; w= a or t

 <400> 8
 ngtcgaswga nawgaa 16

 <210> 9

Second Corrected Sequence Listing 5-2002

<211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide
 n= a, t, g, or c; w= a or t

 <400> 9
 wgtgnagwan canaga 16

 <210> 10
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide
 n= a, t, g, or c; w= a or t

 <400> 10
 wggwancwga wangca 16

 <210> 11
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide
 n= a, t, g, or c; w= a or t

 <400> 11
 wcgwwgawca ngncga 16

 <210> 12
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide
 n= a, t, g, or c; w= a or t

 <400> 12
 wgcnagtnag wanaag 16

 <210> 13
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide

Second Corrected Sequence Listing 5-2002
n= a, t, g, or c; w= a or t

<400> 13
awgcangncw ganata 16

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 14
ctgtacatac tgagtacaat cgga 24

<210> 15
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 15
gcttcaattc ctgcctcagt tgaac 25

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 16
ctctacgtgc ttaacatcat gcga 24

<210> 17
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 17
ccagcttctg ctactagaaa gtcag 25

<210> 18
<211> 25
<212> DNA
<213> Artificial Sequence

Second Corrected Sequence Listing 5-2002

<220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide

 <400> 18
 ctggagttgc atgaaatcct ggatg 25

 <210> 19
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide

 <400> 19
 gctctttgta agctgttcac gagac 25

 <210> 20
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide

 <400> 20
 tcgcatgatg ttaagcacgt agag 24

 <210> 21
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide

 <400> 21
 gagtactggt ccgtgaacag gtaat 25

 <210> 22
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Synthetic
 Oligonucleotide

 <400> 22
 atgcttgac aagcatggc ggaaa 25

 <210> 23
 <211> 25
 <212> DNA

Second Corrected Sequence Listing 5-2002

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 23

tgcaacatcg tgcatttgct ccaga

25

<210> 24

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 24

cacaagcatg agtttttcct tccgg

25

<210> 25

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 25

ctgactttct agtagcagaa gctgg

25

<210> 26

<211> 519

<212> DNA

<213> Brassica oleracea

<220>

<223> seq1-23
n= a, t, g, or c

<400> 26

gaattcctgn	nttacggcat	ccttaataga	ctgttcaa	aat	ggaactcctg	aacctggggt	60
tccactccca	tggaagtgtt	ccagcttata	aaataaatat	gatgcccccc	acatgagcaa		120
tgcatgtgtg	agaggacggg	ttaggttctc	tagaggctta	ttttgcctag	caagaatcag		180
ggttttttct	tcaactgtaa	acactgagta	caaccggaaa	atcttagttc	tttcagaaca		240
cgactcaacc	tttatcttct	ctaagagctt	aacgtcatgc	gatggattca	ggctgcttcc		300
aaaaagtata	aaagactcag	cgcgtaagag	tttaatgctt	tgactacagg	cacgtatttc		360
cagcagcaga	ataaaacact	cactctcctt	gttgaaattg	tttatagcgt	tcttcttcga		420
gaggcagacc	ccatgctcat	aggaattttg	accaaattct	tgcatcagaa	aatcttcgag		480
aatattacca	agcagaagcc	cctcagggct	atgtattgc				519

<210> 27

<211> 419

<212> DNA

<213> Brassica oleracea

<220>

Second Corrected Sequence Listing 5-2002

<223> seq1-27

<400> 27

gaattcagga	tcaaaagggt	tgccggttgg	agaaactggt	ttagagaaag	gctctgattt	60
tcctgtggaa	gtaactaagg	atatagagaa	gacagtgggt	gattcatccc	ccatggttga	120
aactgaggat	ggcagtgtta	taggttcacc	atccgagaat	ccagaaccac	aaaagcttcg	180
tgacagtgaa	actagcttgg	aaaccgatat	agacttggct	ctgaaaagaa	aaagagacac	240
tgcagaaatt	gtgatggatg	catgtacaaa	tgcagatgac	cgcattatga	gtactgatgg	300
ggttattcct	tttcacccg	tgtgcacaaa	tattaatcaa	cccgaagggt	gtggcacatg	360
tcaaaaacgg	caaaagtaag	aatttccgac	tgttgtctgt	cgttttgaaa	ccatttgcc	419

<210> 28

<211> 467

<212> DNA

<213> Brassica oleracea

<220>

<223> seq1-43

<400> 28

gaattctcgt	ccatactttc	ttccgatgtt	ggagaagaaa	atgaaggcaa	gctgtgtcta	60
cttttggaag	ccaagcatgc	tcagggaagt	tacagcactg	atgctactct	atttggtgaa	120
gaacatgtca	agttatcaga	tgaaagtcca	aatatgtttt	ggtcaaagct	gttgagtggg	180
aagaacccta	tgtggaaata	ctgttcggat	actcctcaaa	ggagtcgaaa	aagagtacgg	240
catcttcagg	gctatgagga	gactaccaaa	gttggaatg	gcggaactt	aaagaagaaa	300
aagaaggctt	cagatgatgt	cacagttagat	aacgctgaga	gaaaagcctc	tggaaaggat	360
cacatgggta	aaacagttca	cttcctgctc	ctttacctct	agtgttcatt	gaatgttcca	420
tttactttgc	ttactatctt	tccttcaggg	catttgagat	cacaaa		467

<210> 29

<211> 490

<212> DNA

<213> Brassica oleracea

<220>

<223> seq1-47

<400> 29

gaattcagct	tttaaaactg	atctctgctc	acagataatt	taagagtcag	tgaaaattga	60
gataaaacga	acaaaactg	gaggtaacag	atactctgag	aacaactaac	cttttcttca	120
taagtcttct	ttgtgttctc	tgattctctc	cgcagcttct	ccagttcatg	ctgaaatggg	180
tcactgaaca	cagggaagg	tacttgagga	acaggtggag	tggcattctg	tcccgtagca	240
ttgttaagct	gtgaagaaac	aggagctggt	acacctgctg	gaggctccac	aacaccttca	300
tcgacaacgt	ctgcgtaaaa	ggtattacca	gattgtcagt	ttctctggca	aacacatacg	360
ttatacttaa	atgcaaaaga	gcagttactg	acttgcaaag	gttggttggt	ctacttgagc	420
atcaggttct	gctacttcca	tttcacatgc	ttctgatcca	gttggtgcgag	gcgcagccat	480
tgttgtgttg						490

<210> 30

<211> 515

<212> DNA

<213> Brassica oleracea

<220>

<223> 2-33

<400> 30

tctagagaag	aggtggatta	tgtatatctt	tttctgtact	gcatgaagag	tctattcgtg	60
gggcgcacac	aaggtttcca	agaaaagggt	gaagaatgca	tggctgagaa	aagaggtagc	120
cattatagct	cagtaaccaa	ggatgttgaa	aagactatta	gcgacatcaa	aaagaaatgc	180

Second Corrected Sequence Listing 5-2002

agtaagagcc	tgcataagct	tgtacaaacc	ctcgaggaag	aaaagatgga	cctgatgaat	240
aggaatgctg	tcaagaagca	ggaacttcag	aattgtaaaa	aggtggaagc	atcatttatt	300
cgtgtcacct	attcaggtat	aaatactcag	agcttacatg	atgctctcca	acggctggaa	360
tgtacttttg	aaagaaagtt	tgatgatctc	aaaggagagt	tggatgaatg	ccttgaaagt	420
ttagagcaaa	taaacgaggc	tggaaagaag	aagttggctg	aagatgaagc	ctgttggatt	480
agtcggatag	agaaatgggc	acgagctgaa	ttaag			515

<210> 31
 <211> 574
 <212> DNA
 <213> Brassica oleracea

<220>
 <223> seq2-37

<400> 31						
tctagaccaa	actattaaac	gctaaacata	agaagattag	atcactcgtc	atcagagaga	60
cagaccacat	cattgctcct	ctgcaatcca	ctccccaagt	tctgtggttg	ttcttgctgc	120
tgaataaacg	catttgaata	tggtaaaggg	ttggagatga	gaggttgtct	tggttgaggc	180
attgtgcagt	acggagccga	agcagtatga	ttcctcagtg	cgcttacttg	tgttgctctc	240
tgtgtcagct	gctggattct	aactggagaa	agaaaaaaag	aaaaaaaagg	tgttattatg	300
acttcataac	cttataatctt	taaaaaacaa	ttatgcttct	attattcgaa	cacttgccca	360
ttggagttgc	tgctgaggaa	tgagaggaga	ttctgctcgt	acatttagac	aagaacgcac	420
tcgacaacag	cttgttcttt	ataacaagat	tcttcctcgt	ctgtaacttc	gtctttctgg	480
ctgcatgtac	agcttgatcc	tcatgaaact	ttctctgata	ctcttcttgt	aattcagcta	540
tcttcttctc	gaatttagct	ttcaagactg	cttt			574

<210> 32
 <211> 466
 <212> DNA
 <213> Brassica oleracea

<220>
 <223> seq2-53

<400> 32						
tctagattgt	aatttttaa	ttacaacaaa	ttttgaaagg	gtcagcgatg	agtttgcaaa	60
tctccgtgtt	tcctccagca	ttgctcagcc	agttcaagaa	cctgatcact	tgccacaggt	120
tggtttcttc	ttgctttact	ttggacacct	gtttaatatt	ggcctgtcaa	atttacttat	180
ccttttactt	ctaaactgca	aattctgggtc	tgcattgcat	tgtgatatga	aggtatctgg	240
acccgcttca	agcagagact	atggggagga	caggcagaat	atgcaacaag	ataaatcaca	300
tgaccgaaag	ttgtcatcga	tgatccaga	gtattgggtt	ccagtgcagc	tatcagatgt	360
acagatagag	caatactgtc	ggactctctt	ctccaaatct	tcatctcttt	cttcgctgtc	420
gaggactgat	cctgttctgag	ctcttgaaca	aactctcagt	tctgta		466

<210> 33
 <211> 417
 <212> DNA
 <213> Brassica oleracea

<220>
 <223> seq2-57

<400> 33						
tctagagcaa	ttgaaaccta	attccgattt	tgcgcgggcc	agagattctt	cacggttgaa	60
cttttgctta	acgaaagaga	ctgcaatcca	aatctggaag	tgcattatta	agaacgtatt	120
cagcaatatt	cataaattat	gcaacaatca	aaggccttac	gttgtggcct	acaaagcatg	180
gattttgtta	gatattagta	gctagtctaa	ttcaagcaat	taatggaagt	ttctatccta	240
tgactggaaa	gttaaacatt	cccacaaaag	cagtgatgcc	acagatgatg	aagaagaaaa	300
atgcatatac	tatggaagtg	aatgctatca	taccacagct	atctggaagg	cctgcaatgt	360

Second Corrected Sequence Listing 5-2002

tgtagctggc tctttgcaga cacggtgggt gtcaataata tattcaagaa ctttttc 417

<210> 34

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<222> 1..8

<223> ATP/GTP-binding motif A consensus sequence

<220>

<222> 1

<223> Xaa= Ala or Gly

<220>

<222> 2..7

<223> Xaa= any amino acid

<220>

<222> 8

<223> Xaa= Ser or Thr

<400> 34

Xaa Xaa Xaa Xaa Xaa Gly Lys Xaa

1

5

10

15